U.S. PATENT APPLICATION

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Invention: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
               MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
               EFFECTIVE AS ANTI-MALARIAL COMPOUNDS

SPECIFICATION

AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS EFFECTIVE AS ANTI-MALARIAL COMPOUNDS

5   ## Field of the invention

This invention relates to a new protein encoded in the plastid DNA of the malaria parasite *Plasmodium falciparum*, to DNA encoding the protein, to methods of producing the protein, to methods of screening for anti-malarial compounds, to

10   compounds identified by such screening methods and to methods of preventing or treating growth of the malaria parasite.

Background to the invention

15   The malarial 35 kb circular DNA molecule central to this invention corresponds to a minor species of DNA distinct from nuclear DNA discovered in the 1960s (Gutteridge *et al.* 1971). In the mid-80s the first study on its purification and molecular analysis was published (Williamson *et al.* 1985) . Its similarity was noted to a circular DNA in the related organism *Toxoplasma gondii* - a well known

20   opportunistic pathogen in AIDS cases.

It is important to stress that the malaria parasite and related apicomplexans are unusual amongst non-photosynthetic organisms in that they possess two forms of organellar DNA, typically a property of plants. One form of organellar DNA has

25   been identified as mitochondrial DNA (mtDNA), whereas the other, the 35 kb circle, we have proposed is the remnant of a plastid DNA (plDNA), a provenance hitherto unsuspected for these organisms (Wilson *et al.* 1991, 94). This plDNA was probably acquired by an ancient progenitor of the phylum and may be of algal origin (Williamson *et al.* 1994). The precise location of these organellar DNAs in the cell

30   shows they are in separate compartments (Kohler *et al* 1997).

Thus, there are potentially two organellar protein synthesising systems of independent prokaryotic origin within the malaria organism that could be susceptible to inhibition with antibiotics. Although the malarial mitochondrion is the best characterised of the organelles, its genetic content is highly idiosyncratic,

5   contributing only incomplete fragments of two rRNA genes to the machinery required for protein synthesis. The circular DNA from the putative plastid, on the other hand, is much more conventional, producing transcripts of four complete rRNA genes, some twenty tRNA genes, subunits of a typical plastid RNA polymerase, and a number of ribosomal protein genes organised in modified bacterial operons.

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Summary of the invention

In sequencing the malarial plastid DNA, we found that it contains a gene encoding a new EF-Tu protein homologous to the EF-Tu proteins known in prokaryotes. Thus,

15   the invention provides an EF-Tu protein encoded on the plastid DNA of the malaria parasite *Plasmodium falciparum*. The invention also provides DNA encoding the protein.

The prokaryotic EF-Tu proteins are known to be important in controlling the

20   elongation cycle in protein synthesis, and it is known that inhibition of the proteins by various compounds has an antibiotic effect. In view of the sequence similarity between the prokaryotic EF-Tu proteins and our newly-identified malarial plastid EF-Tu protein, we proposed the theory that the antibiotic compounds which inhibit the prokaryotic proteins may also inhibit the malarial protein and therefore be useful

25   as anti-malarials. We tested such antibiotics (e.g. kirromycin and aurodox) for their anti-malarial effect and found our theory was correct; the antibiotics were found to be effective anti-malarials both *in vitro* and *in vivo*. Thus, the invention provides a method of preventing or treating infection of a patient with the malaria parasite *Plasmodium falciparum*, which method comprises administering to the patient a

30   compound which inhibits the EF-Tu protein encoded on the plastid DNA of said malaria parasite.

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The knowledge provided by the invention of the EF-Tu protein in the malaria plastid and the fact that its inhibitors are effective anti-malarials allows the protein to be used in screening for new anti-malarial compounds. Accordingly, the invention includes a method of identifying an anti-malarial compound, which method

5   comprises

(i) contacting a test compound with the EF-Tu protein encoded on the plastid DNA of the malaria parasite *Plasmodium falciparum*; and

10   (ii) determining whether the compound binds to or inhibits the protein, any such binding or inhibition being indicative that the compound is an anti-malarial.

We also investigated the ability of antibiotics which bind to other components of the

15   prokaryotic protein synthesis machinery to act as anti-malarial compounds. As a result of these investigations, it was found that thiostrepton, which is known to bind to the GTPase domain of the 23S ribosomal RNA of *E. coli*, is also able to bind to GTPase domain of the 23S rRNA encoded on the plastid of the malaria parasite *Plasmodium falciparum* (Pf 23S rRNA$_{pl}$). Accordingly, the invention provides a

20   method of identifying an anti-malarial compound, which method comprises

(i) contacting the compound with the 23S ribosomal RNA encoded on the plastid DNA of the malaria parasite *Plasmodium falciparum* (Pf 23S rRNA$_{pl}$) or with a fragment of said RNA containing the GTPase domain; and

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(ii) determining whether the compound binds to said RNA or said fragment, any such binding being indicative that the compound is an anti-malarial.

Brief description of the drawings

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Figure 1 is a schematic illustration of the elongation cycle that occurs during protein

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synthesis and shows the points in the cycle at which various inhibitors operate.

Figure 2A shows the amino acid sequence of the EF-Tu protein according to the invention from the plastid of the malaria parasite *Plasmodium falciparum* (pf). The sequence is aligned with sequences of EF-Tu proteins from other organisms, namely *E. coli* ("ecoli"), *Anacystis nidulans* ("anani"), *Cyanophora paradoxa* ("cypha") and *Cryptomonas phi* ("cryph").

Figure 2B shows the nucleotide sequence of the *tufA* gene that encodes the EF-Tu protein according to the invention.

Figure 3A shows a Southern blot of endonuclease-restricted malarial genomic DNA hybridised with a Pf*tufA*-specific PCR product as probe. A single band for the 35 kb plastid was obtained for each restriction digest.

Figure 3B shows cross-hybridisation between endonuclease-restricted malarial genomic DNA and the yeast *tufM* gene, indicating the possible presence of a malarial version of *tufM*.

Figure 4 shows the results of an experiment in which an antisense RNA probe (about 230nts) made by *in vitro* transcription, corresponding to a portion of the *tufA* gene encoding domains I and II of the predicted EF-Tu$_{pl}$ protein, was used in an RNase protection assay to demonstrate the presence of *tufA* transcripts in total RNA extracted from erythrocytic parasites during the course of a single growth cycle (0-40 hrs).

Figure 5 shows dose-response curves for the effects of fusidic acid, mocimycin (kirromycin), thiostrepton and GE 2270 on incorporation of ^{3}H-hypoxanthine and ^{14}C-isoleucine into erythrocytic stages of *P. falciparum* grown in cultures over a 36 hour period. The Figure also shows a dose-response curve for the effect of mocimycin on myeloma cells (a control).

Figure 6 shows the effects of aurodox and mocimycin on the growth of *P. chabaudi* in mice. The solid line is for aurodox, the dotted line is for mocimycin and the dashed line is for no drug controls. The arrows on the x-axis indicate days on which three 0.1 ml 100mM ip injections were given.

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Figure 7 shows the sequence of the GTPase region of the plastid 23S rRNAs of *Plasmodium falciparum* (Pf) and *Toxoplasma gondii* (Toxo) (numbers based on *E.coli*), showing substitution sites (circled) affecting the binding of thiostrepton. The alternative nucleotides in Pf cytosolic 28S rRNA and Pf mitochondrial 23S rRNA are

10   indicated.

Figure 8 shows thiostrepton titrations (means of duplicates, bar = range) in a filter binding assay with transcripts of the GTPase region of LSU rRNA.

A) Short 23S transcripts of *P.falciparum* (Pf) wild type rRNA$_{pl}$ (open circle A1067)

15   and mutated forms (open square A1067U and filled triangle A1067G), as well as Pf 28S rRNA transcripts (filled square), are compared with an optimized *E.coli* control transcript (filled circle). For convenience, nucleotide numbers correspond to *E.coli*. B) *T. gondii* wild type rRNA$_{pl}$ transcript (filled triangle) and mutated transcript (open triangle) compared with control transcripts from *P.falciparum* rRNA$_{pl}$ (open circle)

20   and *E.coli* (filled circle).

Figures 9 and 10 show the structures of various antibiotics usable in the invention.

Figure 11 shows slot blots of RNA fractioned on sucrose gradients. Pretreatment

25   with anisomycin blocked the puromycin-induced shift of the hybridization signal for *P.falciparum* cytosolic 23S ribosomes but not the plastid 16S ribosomes.

A-C. Blots hybridized with a probe for the cytosolic large subunit (23S) rRNA. Anisomycin blocked the puromycin-induced shift.   —

D-F. The same blots hybridized with a probe for the plastid-encoded small subunit

30   (16S) rRNA. Anisomycin did not block the puromycin-induced shift.

Figure 12 is a slot blot showing the puromycin-induced shift of the hybridization signal for plastid mRNA specifiying EF-Tu.

Figure 13 contains immunoblots showing that binding of antibiotics modifies migration of EF-Tu.GDP in native polyacrylamide gels. Two segments of the same gel show A) heterologously expressed Pf EF-Tu$_{pl}$ protein detected with a malaria peptide-specific antibody and B) *E.coli* EF-Tu detected with a specific antibody (Breidenbach et al 1990). Lanes without antibiotics (1 and 5), lanes with 100μM antibiotic: GE2270A (2 and 6), enacyloxin lla (3 and 7), kirromycin (4 and 8). Arrows indicate uncomplexed EF-Tu.

Detailed description of the invention

The EF-Tu protein

The function of the EF-Tu protein is in the elongation cycle of protein synthesis. The cycle is illustrated in Figure 1. EF-Tu reacts with GTP and AA-tRNA to form an EF-Tu/AA-tRNA/GTP complex. After binding to EF-Tu, the AA-tRNA component is transferred to the ribosomal A site with the release of free EF-Tu-GDP complex and phosphate. The GDP is released from EF-Tu and the EF-Tu is then ready for another cycle.

EF-Tu is an exceedingly abundant protein in *E. coli*, present in approximately as many copies as there are tRNA molecules. It can bind every tRNA except for fMet-tRNA.

The malarial plastid EF-Tu has much sequence identify with known EF-Tu proteins from other organisms (see Figure 2A). We have made a 3D-model structure for the malarial plastid EF-Tu protein based on the crystal structures available for bacterial equivalents (*E. coli* and *T. thermophilus*). This model showed that the bacterial and malarial proteins are very similar indeed, strongly implying that the malarial plastid

EF-Tu is functional.

The sequence of the malarial plastid EF-Tu protein of the invention may be that labelled "eftu_pf" in Figure 2A, but variations in this sequence are possible. The protein may, for example, have a sequence identity with the sequence in Figure 2A of 80% or more, 90% or more, 95% or more or 99% or more.

The sequence of Figure 2A may be modified by substitution, deletion, extension or insertion. A substitution, deletion or insertion may involve one or more amino acids, typically from 1 to 5, from 1 to 10 or from 1 to 20 amino acids.

Such modified sequences must retain the functions of the EF-Tu protein necessary for participation in the elongation cycle of protein synthesis. In general, the physicochemical nature of the sequence of Figure 2A should be preserved; the amino acids of a modified sequence should generally be of a similar charge, size and hydrophobicity/hydrophilicity as those in the sequence of Figure 2A. Candidate substitutions are those in which an amino acid from one of the following groups is replaced by a different amino acid from the same group:

- H, R and K
- I, L, V and M
- A, G, S and T
- D and E.

The EF-Tu protein of the invention may be provided in purified form. The protein may also be provided in pure form and in isolated form. The protein may, for example, be provided in a preparation in which it constitutes 10% or more, 40% or more, 80% or more, 90% or more, 95% or more or 99% or more of the total protein in the preparation by weight.

The protein will usually be obtained by expression of recombinant DNA containing

the protein, but may also be obtained by biochemical purification of the protein from
the malaria parasite.

DNA encoding the malarial plastid EF-Tu protein

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The DNA encoding the EF-Tu protein may have the sequence shown in Figure 2B,
but variations in this sequence are possible. The DNA molecule may, for example,
have a sequence identity with the sequence shown in Figure 2B of 70% or more, 80%
or more, 90% or more, 95% or more or 99% or more.

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A recombinant DNA molecule encoding the EF-Tu protein of the invention may be
obtained using well-known and conventional recombinant DNA techniques, such as
those described in Sambrook *et al* (1989) Molecular Cloning: A Laboratory Manual,
2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

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Such DNA molecules may be obtained by making a library of replicable expression
vectors. The library may be created by cloning all the DNA or, more preferably, the
plastid DNA of the malaria parasite into a parent vector. The library may be
screened for members containing the desired nucleic acid sequence, e.g. by means of
20   a DNA probe or antibody.

The term "replicable expression vector" is used herein to mean a vector which
contains the appropriate origin of replication sequence for directing replication of the
vector. The vector may also contain the appropriate sequences for expression of the
25   EF-Tu protein. The sequences for expression of the protein will generally include a
transcription promotor and a translation initiator operably linked to the coding
sequence. The term "operably linked" refers to a linkage in which the promotor and
initiator are connected in such a way to the coding sequence as to permit expression
of the protein. A vector may, for example, be a plasmid, virus or phage vector. A
30   vector may contain one or more selectable markers, for example an ampicillin
resistance gene in the case of a bacterial vector or a neomycin resistance gene in the

case of a mammalian vector. A foreign gene sequence encoding the EF-Tu protein inserted into a vector may be transcribed *in vitro* or the vector may be used to transform a host cell.

5   According to one embodiment of the invention, there is provided a host cell transformed with a vector encoding the EF-Tu protein. A vector and host cell will be chosen so as to be compatible with each other, and may be prokaryotic or eukaryotic. A prokaryotic host may, for example, be *E.coli* in which case the vector may, for example, be a bacterial plasmid or a phage vector. A eukaryotic host may, for

10   example, be a yeast (e.g. *S.cerevisiae*), a chinese hamster ovary (CHO) cell or an insect cell (e.g. *Spodoptera frugiperda*).

The invention includes a method of producing the EF-Tu protein encoded on the plastid DNA of the malaria parasite *Plasmodium falciparum*, which method

15   comprises

        (i) culturing a host cell containing a DNA molecule encoding the protein under conditions such that the protein is expressed; and

20   (ii) recovering the protein from the culture.

Antibodies to the malarial plastid EF-Tu protein

The invention includes an antibody specific for the EF-Tu protein of the invention.

25   The antibody is preferably monoclonal, but may also be polyclonal. The antibody may be labelled. Examples of suitable antibody labels include radiolabels, biotin (which may be detected by avidin or streptavidin conjugated to peroxidase), alkaline phosphatase and fluorescent labels (e.g. fluorescein and rhodamine). The term "antibody" is used herein to include both complete antibody molecules and fragments

30   thereof. Preferred fragments contain at least one antigen binding site, such as Fab and F(ab')₂ fragments. Humanised antibodies and fragments thereof are also

included within the term "antibody".

The antibody may be produced by raising antibody in a host animal against an EF-Tu protein according to the invention or an antigenic epitope thereof (hereinafter "the immunogen"). Methods of producing monoclonal and polyclonal antibodies are well-known. A method for producing a polyclonal antibody comprises immunising a suitable host animal, for example an experimental animal, with the immunogen and isolating immunoglobulins from the serum. The animal may therefore be inoculated with the immunogen, blood subsequently removed from the animal and the IgG fraction purified. A method for producing a monoclonal antibody comprises immortalising cells which produce the desired antibody. Hybridoma cells may be produced by fusing spleen cells from an inoculated experimental animal with tumour cells (Kohler and Milstein, Nature 256, 495-497, 1975).

An immortalized cell producing the desired antibody may be selected by a conventional procedure. The hybridomas may be grown in culture or injected intraperitoneally for formation of ascites fluid or into the blood stream of an allogenic host or immunocompromised host. Human antibody may be prepared by *in vitro* immunisation of human lymphocytes, followed by transformation of the lymphocytes with Epstein-Barr virus.

For the production of both monoclonal and polyclonal antibodies, the experimental animal is suitably a goat, rabbit, rat or mouse. If desired, the immunogen may be administered as a conjugate in which the immunogen is coupled, for example via a side chain of one of the amino acid residues, to a suitable carrier. The carrier molecule is typically a physiologically acceptable carrier. The antibody obtained may be isolated and, if desired, purified.

Assays for identifying anti-malarial compounds that inhibit the malarial plastid EF-Tu protein

As mentioned above, the knowledge provided by the invention of the EF-Tu protein
in the malaria plastid and the fact that its inhibitors are effective anti-malarials allows
the protein to be used in screening for new anti-malarial compounds.

Various different assay systems may be used to carry out the screening, but all the
assays have in common that the EF-Tu protein of the invention is contacted with test
compounds and the ability of each test compound to bind to or inhibit the protein is
determined. Any such binding or inhibition is indicative that the compound could be
useful as an anti-malarial drug.

The screening assays will generally require one or more controls. It will generally be
desirable to include a positive control in the form of a compound known to bind to or
inhibit the EF-Tu protein, so as to ensure that the assay system is responding
properly. Examples of suitable positive controls include kirromycin (mocimycin)
and aurodox (1-methylmocimycin), which we have shown through our experiments
to be effective anti-malarials and which are known to inhibit prokaryotic EF-Tu. It
will also generally be desirable to include a negative control in the form of a sample
containing no test compound, so as to obtain a measurement of the background
signal in the assay. If a test compound gives a signal in the assay above that of the
background, this is indicative that the compound has given a positive result and
could be an anti-malarial.

One convenient type of assay system is a "band shift" system. This involves
determining whether a test comopund advances or retards the EF-Tu protein of the
invention on gel electrophoresis relative to the EF-Tu protein in the absence of test
compound. The mobility of GDP complexed EF-Tu is decreased with GE2270A but
increased with enacyloxin IIa or kirromycin.

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Another convenient type of assay system is a competitive binding system. Such a system may comprise

     (i) incubating the EF-Tu protein of the invention with a test compound and a labelled reference compound that is known to bind the protein (e.g. kirromycin or aurodox);

     (ii) determining the amount of the labelled reference compound that is bound to the protein; and

     (iii) comparing the amount of bound labelled reference compound determined in step (ii) with the amount of said compound that binds to the protein in the absence of the test compound;

wherein any reduction in the binding of the labelled reference compound in the presence of the test compound compared to the binding in the absence of the test compound shows that the test compound is competing with the reference compound for binding to the protein and indicates that the test compound could be an anti-malarial.

The amount of the labelled reference compound bound to the protein may be measured directly or indirectly. A direct measurement may be carried out by removing assay mixture containing the unbound labelled reference compound and measuring the amount of label that is in the protein fraction. Alternatively, the amount of labelled reference compound bound to the protein could be determined indirectly by measuring the amount of label remaining in the assay solution after removal of the protein fraction, which will be inversely related to the amount that has bound to the protein.

In a competitive binding assay system, the EF-Tu protein may be immobilised on a solid support or may be in solution. The use of immobilised protein has the

advantage that, after the binding reaction is complete, the protein/labelled reference compound complex may be separated from the labelled reference compound that remains in solution by simply removing the solution away from the solid support. If, on the other hand, the protein is not immobilised during the assay but rather is in solution, then it will generally be necessary to devise a means for separating the protein/labelled reference compound complex from the uncomplexed reference compound before measuring the amount of label. Such separation could be achieved, for example, by precipitating the protein using an antibody to the protein or by using a non-specific protein precipitation technique.
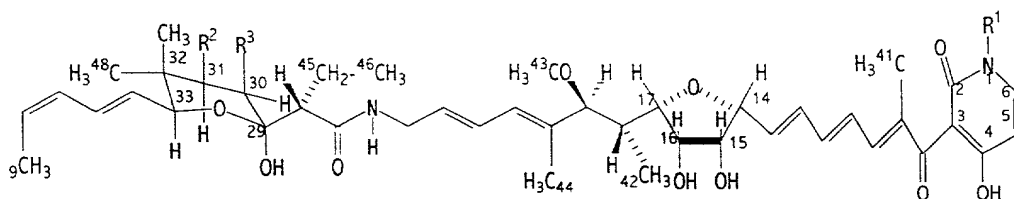
Suitable labels for use in the assay systems according the invention are well-known in the art and include the labels set out above that may be attached the antibodies of the invention.

Use of compounds that inhibit the malarial plastid EF-Tu protein as anti-malarials

Compounds that inhibit the malarial plastid EF-Tu protein may be used as antimalarial compounds. Such compounds may be identified using the screening assays described above.
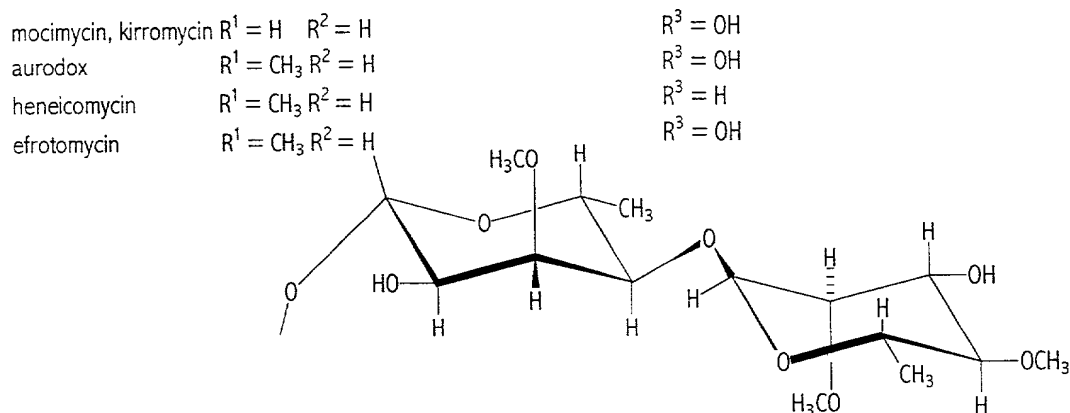
We have already identified some such compounds, e.g. the antibiotics kirromycin (mocimycin), aurodox (1-methylmocimcyin), Efrotomycin (a glycoside of kirromycin), Enacyloxin IIa and GE2270. Efrotomycin has previously been shown to have the desirable properties of rapid oral absorption and prolonged plasma half-life.

The antibiotics in the kirromycin series may be represented by the general formula:

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wherein R^1 is hydrogen or a C_1-C_4 alkyl group (e.g. methyl); R^2 is hydrogen, C_1-C_4 alkyl or a sugar group (e.g. a disaccharide); and R^3 is hydrogen, OH or C_1-C_4 alkyl.

Preferred antibiotics for use in the invention are as follows:

mocimycin, kirromycin	$R^1 = H$	$R^2 = H$	$R^3 = OH$
aurodox	$R^1 = CH_3$	$R^2 = H$	$R^3 = OH$
heneicomycin	$R^1 = CH_3$	$R^2 = H$	$R^3 = H$
efrotomycin	$R^1 = CH_3$	$R^2 = H$	$R^3 = OH$

The compounds may be used in either the treatment of an existing infection by the malaria parasite or in the prevention of such an infection from occurring in the first place. The dosage regimen will ultimately be at the discretion of the physician, who will take into account factors such as the nature of the compound, the severity of any disease and the weight and age of the patient. However, suitable routes of administration may include the oral route, the rectal route, the intramuscular route and the intravenous route. The oral route is preferred because this is generally the most convenient route for a patient to take regular doses of the compound without the assistance of a physician. A typical dose would be from 1 to 1000 mg and such a dose may, for example, be taken from 1 to 3 times daily.

In order to be administered to a patient, the compound will be provided in the form of a pharmaceutical composition containing the active compound and a pharmaceutically acceptable carrier or diluent. Typical oral dosage compositions include tablets, capsules, liquid solutions and liquid suspensions.

Compounds that bind to the 23S rRNA encoded on the malaria parasite

We have found that the 23S rRNA encoded on the plastid of the malaria parasite *Plasmodium falciparum* (Pf 23S rRNA$_{pl}$) is a target for compounds with anti-malarial activity. More specifically, we have found that the mechanism of action of the antibiotic thiostrepton, which was known to have anti-malarial activity, is through binding to the GTPase domain of the 23S rRNA of the malaria plastid.

This information allows the design of assays for screening for further anti-malarial compounds whose mechanism of action operates through the 23S rRNA. These assays involve contacting each of the test compounds with the 23S rRNA or a fragment thereof containing the GTPase binding domain, and measuring any binding of the test compounds to the rRNA or fragment. Any such binding is of course indicative that the compound could be an anti-malarial.

We have already developed one assay for detecting binding to the 23S rRNA. We made a short transcript from DNA encoding the 23S rRNA of the malaria plastid corresponding to the GTPase domain (about nucleotide 1051 to about nucleotide 1108) and found that the transcript bound thiostrepton strongly.

The binding was specific. It depended to a large extent on the presence of an A residue at the position corresponding to *E. coli* position 1067. A transcript corresponding to the GTPase domain of the *E. coli* 23S rRNA (which contained the A at position 1067) was also shown to bind thiostrepton strongly. Mutation of A1067 to either U or G in the malaria plastid transcript dramatically reduced binding. A transcript corresponding to the GTPase domain of the <u>cytosolic</u> malaria 28S rRNA also bound thiostrepton poorly.

A screening assay for further anti-malarial compounds can be based on a competitive binding assay in which the ability of each test compound to compete with thiostrepton for binding to the Pf 23S rRNA$_{pl}$ is measured. Such an assay comprises

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(i) incubating the Pf 23S rRNA$_{pl}$ or a fragment thereof containing the GTPase domain with the test compound and thiostrepton as a reference compound (or another reference compound known to bind to the rRNA or the fragment);

5   (ii) determining the amount of thiostrepton (or other reference compound) that is bound to the rRNA or the fragment; and

(iii) comparing the amount of thiostrepton (or other reference compound) bound to the rRNA or the fragment with the amount that is bound in the
10   absence of the test compound;

wherein any reduction in the binding of the thiostrepton (or other reference compound) in the presence of the test compound compared to the binding in the absence of the test compound is indicative that the test compound is competing for
15   binding to the rRNA and that the test compound could be an anti-malarial.

In a screening assay based on the invention for further anti-malaria compounds, it would be necessary to use appropriate controls. A good positive control would be to use a compound known to compete with thiostrepton (or with the other reference
20   compound) to ensure that the assay is working properly; a positive result for the known competitor in the assay would indicate that the assay had worked correctly. It would also generally be desirable to use a negative control comprising, for example, a sample in which no thiostrepton or test compound is present; this would enable the background signal in the assay to be determined and any signal above the
25   background would indicate binding to the 23S rRNA.

The following experiments serve to illustrate the invention.

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EXPERIMENTAL SECTION

Materials and Methods

5   *Polysome preparation and puromycin shift - P.falciparum* was grown in blood
cultures (Trager et al 1976) and ribosomes prepared as described (Sherman et al
1975). Parasitized erythrocytes were lysed for 1 hr on ice in a buffer containing
0.14% Nonidet P-40 (Trade Name), 25mM KCl, 10mM $MgCl_2$, 380mM sucrose,
6.5mM β-mercaptoethanol and 50mM Tris HCl, pH 7.6. The lysate was centrifuged

10   x3 at 10,000g for 10 min at 4°C to remove genomic DNA and other cell debris
before further centrifugation at 105,000g for 1 hr in an SW40 rotor (Trade Name,
Beckman) at 4°C. The resulting pellet was resuspended in 25mM KCl, 5mM $MgCl_2$
and 50mM Tris HCl (pH 7.6) and homogenized by hand (x50 strokes) with a glass
dounce homogenizer (Wheatstone, USA). The suspension was centrifuged at

15   10,000g for 10 min at 4°C and the crude pellet discarded before further
centrifugation for 2 hr at 105,000g in an SW55 rotor (Beckman) at 4°C. The pellet
was resuspended in 10mM Tris HCl, 10mM $MgCl_2$, 100mM KCl and homogenized
again to give a suspension of ribosomes.

20   Polysomes were fractioned on sucrose gradients (20-50% w/v) prepared in 0.3M
KCl, 3mM $MgCl_2$ and 1mM dithiothreitol (DDT) with 0.02M Tris HCl (pH 7.6) -
referred to as "high salt" buffer; centrifugation was at 30,000g (Beckman Sw40 rotor)
for 21 hr at 4°C.

25   In an experiment with RNase (Cox 1969), total polysomes were incubated with a
range of concentrations of RNase (1-13ng ml^{-1} ribosomes, Boehringer) prior to
centrifugation for 30 min at 26°C. In other experiments, polysomes were dissociated
to monosomes and subunits by the incorporation of puromycin; here the total
ribosome preparation was incubated for 20 min at 37°C with 2mM puromycin in the

30   "high salt" buffer to which was added 2mM GTP, 10 $\mu l m l^{-1}$ RNAsin (39 $U\mu l^{-1}$,
Promega) and 1mM DTT. In some experiments, ribosomes were incubated with

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both anisomycin (Sigma) and puromycin. Anisomycin was added at 3mM for 10 min at 37°C followed by incubation with puromycin as above (Cundliffe et al 1974). After ribosome fractionation on the sucrose gradients, RNA was extracted with phenol/chloroform/isoamyl alcohol (Chomczynski it al 1987), precipitated in ethanol and blotted on to nylon membranes (Gene Screen, Trade Name) using a slot-blot apparatus (Scot-Labs). Hybridization was carried out with ^{32}P-labelled DNA prepared from either cloned fragments of the 35 kb plDNA of *P.falciparum*, PCR products amplified from it, oligonucleotides based on its sequence (Wilson et al 1996), or with PCR products based on the sequence of Pf 28S cytosolic rRNA (McCutchen et al 1988). Hybridization signals were quantitated using a Molecular Dynamics phosphor imager.

Antibiotics - Samples of Mocimycin (kirromycin), Aurodox (N-methylated kirromycin), and Efrotomycin (a glycoside of kirromycin) were used. Aurodox was dissolved in RPMI-Albumax medium (Grande et al 1977), kirromycin was dissolved in RPMI made alkaline by addition of 1M NaOH, and efrotomycin was dissolved in ethanol before dilution in culture medium. Enacyloxin IIA was dissolved in 1% NaHCO$_3$ prior to dilution in RPMI-Albumax medium. The antibiotic GE2270A was dissolved in 100% DMSO before dilution in culture medium. Fusidic acid (Sigma) was dissolved directly in culture medium, and thiostrepton (Sigma) in 100% DMSO before dilution in culture medium. A hemisuccinate form of thiostrepton was prepared as a potassium salt, according to Bodanszky et al 1965. Incorporation of radiotracers by *P.falciparum* growing in blood cultures in the presence and absence of drugs was carried out as described (Strath et al 1993)

EF-Tu model - Pf EF Tu$_{pl}$ was modelled by homology with the known 3D structures determined by X-ray crystallography of EF-Tu.GTP (Berchtold et al 1993) and EF-Tu.GDP (Polekhina et al 1996) both from *Thermus aquaticus*. Modelling was carried out with the WHAT-IF program package (Trade Name, Vriend 1990), as described in Tews et al 1996. Alignments had to be adjusted manually because of small gaps and insertions. An iterative procedure of the automated model-building

algorithm checked and corrected the alignments until no errors were detectable. Threee insertions in the Pf EF-Tu$_{pl}$ sequence had to be deleted: Leu 190, Pro263 and Leu359 - Val363. The final alignment with the *T. aquaticus* structure had single residue gaps in the Pf sequence between Leu41 and Ser42 as well as residues Asn209

5   and Ile210. Co-ordinates for the C (alpha) backbone were copied from the known structure for overlapping segments and the atoms for the amino acids Gly, Ala and Pro were placed directly in their calculated positions. All remaining residues were assigned to Ala before the order in which side changes had to be placed was calculated by the algorithm implemented by the program. Atoms were subsequently

10   placed using a position-dependent amino acid rotamer library. The model was refined geometrically and re-numbered according to the *P.falciparum* sequence.

Heterologous expression - The malarial plastid *tufA* gene was amplified by PCR, cloned into the TA vector (Trade Name, Invitrogen) and its sequence determined

15   (Wilson et al 1996). Re-cloning into the expression vector pGEX (Trade Name, Pharmacia) was carried out with a PCR product generated using 5' and 3' primers providing custom-made restriction sites. Transfectants in *E.coli* (strains DH5 alpha, Sure, JM109) were found mostly to carry deletions within the *tufA* sequence, but one clone in JM109 contained the complete insert (sequenced on a single strand). This

20   was expressed as a fusion protein of the expected size by induction of mid-log phase cultures with 50µM isopropyl-β-D-thiogalactoside (IPTG) at 37°C or 27°C. The insoluble fusion protein was solubilized in 5M guanidinium HCl and refolded by dilution (Lin et al 1991).

25   *Antibody to an epitope of Pf EF-Tu* - A rabbit polyclonal antibody was prepared against a 13-mer synthetic peptide IQKNKDYELIKSN from domain I of Pf EF-Tu coupled to polylysine beads (Severn Biotech. Ltd). In Western blots (ECL protocol, Amersham), this antibody did not cross-react with EF-Tu from *E.coli*, nor did an antibody to *E.coli* EF-Tu react with the expressed malarial protein.

30

Drug binding - Thiostrepton binding to short rRNA transcripts generated *in vitro* was

assayed according to Ryan et al 1991, as modified by Clough et al 1997. A band
shift method in native 12% polyacrylamide gel (Cetin et al 1996) was used to
demonstrate complex formation between a resolubilized fraction of the expressed Pf
EF-Tu$_{pl}$ and various antibiotics. Before electrophoresis and immunoblotting,
samples were incubated on ice for 15 mins in 50 mM imidazole acetate (pH 7.6), 10
mM NH$_4$Cl, 10mM MgCl$_2$, 1mM DDT and 100μM GDP, in a final volume of 20μl.

Results

Evidence for plastid protein synthesis

Ribosomes from erythrocytic parasites were fractionated by centrifugation on linear
gradients (20-50% sucrose) and RNA was extracted from fractions collected over the
length of the gradients. Slot blots of the RNA were hybridized with ^{32}P-labelled
DNA probes prepared from either cloned fragments of Pf plDNA, PCR products
based on its sequence, or kinased oligonuceotides. As shown in Fig. 11 C&F,
hybridization with probes for the large $_{(cytosolic)}$ or small $_{(plastid)}$ subunit rRNAs gave
signals extending to the bottom of the gradient, indicative of rRNA incorporated in
polysomes. Supportive evidence was obtained by limited digestion of the total
ribosome preparation with RNase (13 ng RNase/mg ribosomes for 30 min at 26°C)
before fractionation - this causes dissociation of the polysomes (Cox 1969) and
shifted the hybridization signal up the gradient (data not shown). More specific
evidence for a subset of polysomes belonging to the plastid compartment was
obtained by incubating total ribosomes with 2mM puromycin in the presence of
GTP, 0.3M KCl and 1mM DDT prior to density gradient fractionation: puromycin
acts as an analogue of the 3' terminal adenosine of aminoacylated tRNAs and is
incorporated into nascent peptide chains, terminating translation and dissociating
polysomes (Gale et al 1981). Incubation with puromycin caused a shift of both the
cytosolic and plastid rRNA hybridization signals up the gradient (Fig. 11, B&E).
The specificity of the puromycin-shift was confirmed by pre-treating Pf ribosomes
with the antibiotic anisomycin which binds only to eukaryotic ribosomes and

prevents puromycin incorporation (Gale et al 1981). As shown in Fig. 11A, anisomycin blocked the puromycin-induced shift of the hybridization signal for Pf 28S cytosolic rRNA, whereas hybridization of the same blot with a probe for Pf 16S rRNA$_{pl}$ showed the puromycin-shift of the plastid subset of polysomes was not

5 blocked (Fig. 11D).

Similar results were obtained with a probe for an mRNA specified by the plDNA. Fig 12 shows the puromycin-induced shift of the hybridization signal for mRNA specifying EF-Tu$_{pl}$.

10

To quantitate the relative proportions of the hybridization signals generated by different species of RNA, slot blots were hybridized with ^{32}P-labelled oligonucleotides, known amounts of DNA being used as appropriate standards. The 28S cytosolic rRNA was estimated to be 80-fold more plentiful than 16S rRNApl

15 and 2000-fold more plentiful than the mRNA specifying EF-Tu$_{pl}$ (data not shown). These results and the puromycin-shifts are consistent with the presence of actively translating plastid ribosomes in blood cultures of malaria parasites.

tufA sequence

20

From a combination of cloned DNA fragments and PCR products amplified from the 35 kb circular DNA of *P.falciparum*, we derived a 1.23 kb nt sequence whose predicted peptide (calculated M.Wt. 46,633) is homologous to the elongation factor EF-Tu (Fig. 2A). The malarial gene lies 45 nts downstream from two ribosomal

25 protein-encoding genes, *rps12* and *rps7*. In this respect, the organization resembles the *str* operon on the plDNAs of the flagellate protists *Euglena gracilis* (Montadon & Stutz, 1984; Hallick *et al.* 1993) and *Astasia longa* (Seimelster *et al.* 1990), as well as the non-chlorophyte alga *Cryptomonas* (Douglas, 1991), and the cyanelle of *Cryptomonas paradoxa* (Kraus *et al.* 1990), the intervening *fus* gene encoding EF-G

30 in the *str* operon of bacteria such as *E.coli* (Zengal and Lindahl BBA 1050, 317 (1990)) presumably having been transferred to the nucleus. The short intergenic

region upstream of the Pfpl*tufA* gene does not contain an open reading frame or putative leader sequence. At the nt level, the malarial pl*tufA* gene is extremely rich in adenine and thymine (A+T) residues (79%) compared to related sequences in the database, a feature with important consequences for computations intended to

5   establish the gene's phylogenetic relationships.

At the predicted peptide level, the malarial sequence is very divergent from other recorded EF-Tu's (only 45% amino acid identity with *E.coli* and 51% identity with *Anacystis nidulans*). Nonetheless, several highly conserved regions are evident,

10   including the four segments of domain I involved in GTP binding. In *E.coli*, the first three of these segments carry the consensus elements G18HVDHGK24; D80CPG83; and N135KCD138. In the malarial sequence there is only one substitution C136E. Most of the residues defining the GDP binding pocket also are conserved (in *E.coli* G23, N135, K136, D138, S173, L175), the only substitution in the malarial sequence

15   being M139L. In a less well conserved region (amino acids 180-190, topologically close to the GTP binding domain), the malarial sequence has an insertion typical of plastid versions of EF-Tu that is not found in the *E.coli* gene, and is only partially present in the mitochondrial equivalent (*tufM*) of *Saccharomyces cerevisiae* (Nagata *et al*. 1983). Despite the gene's high A+T content, the predicted malarial EF-Tu

20   peptide is one of the most highly conserved proteins encoded by the 35 kb circle; however, it is potentially more basic (calculated pI=8.43) than the versions present in bacteria or the yeast mitochondrion (Piechulla & Kuntzel, 1983).

In view of the unknown functional status of the 35 kb circular DNA, it was of

25   interest to compare the predicted malarial EF-Tu$_{pl}$ peptide with the unusual chloroplast form in the Charophycean alga *Colochaete orbicularis*, as it has been suggested that the latter may no longer be functional, there being multiple *tufA*-like sequences in the nucleus (Baldauf *et al*. 1990). Baldauf and colleagues pointed out that the *C.orbicularis* EF-Tu $_{pl}$ amino acid sequence differs in twenty two sites that

30   otherwise are conserved in all but four of 27 other EF-Tu sequences. Despite the malarial gene's extreme A+T content, the predicted EF-Tu peptide has only 6

conservative amino acid substitutions in the same 22 residues (Table 1). This suggests that the functional domains encoded by the *tufA* gene on the 35 kb circle have been maintained under selective pressure.

TABLE 1

AMINO ACID SEQUENCE COMPARISON OF CONSENSUS SITES

(MODIFIED FROM BALDAUF *ET AL.* 1990)

Site*	C	cp	eub	all	Pf
21-22	FS	VD	VD	VD	VD
60-62	NMS	GIT	GIT	GIT	GIT
87	N	D	D	D	D
90	N	K	K	K	K
128	I	V	V	V	V
153	N	E	E	E	E
210	L	I	I	I	I
227	R	D	D	D	D
233	S	G	G	G	G
236	L	T	T	T	T
241	T	R	R	R	K
248	N	K	K	K	N
272	K	E	E	E	E
286	D	N	N	N	N
301	K	R	R	R	R
372	E	D	D	D	D
393	V	A	A	A	S
401	I	V	V	V	I
405	I	V	V	V	I

*   = Amino acids numbered as in Fig. 2A.

C   = *Coleochaete orbicularis* chloroplast *tuf A* (Baldauf *et al.* 1990)

cp   = cyanobacteria and chloroplast consensus

eub = eubacteria, cyanobacteria and chloroplast consensus

all = eubacteria, eukaryotes and archaebacteria consensus

Pf   = *Plasmodium falciparum* 35 kb circule *tufA*

When hybridized with a Pf*tufA*-specific PCR product under stringent conditions, Southern blots of endonuclease-restricted malarial genomic DNA gave a single band of the size predicted (Fig. 3A). At low stringency no other bands were revealed that might have corresponded to the nucleus-encoded mitochondrial gene *tufM* (Nagata *et al*, 1983; Wells *et al*. 1994). The likely presence of a malarial equivalent was indicated, however, by cross-hybridization at low stringency with a PCR product based on the yeast *tufM* gene (Fig. 3B).

An antisense RNA probe (~230nts) made by *in vitro* transcription, corresponding to a portion of the malarial *tufA* gene encoding domains I and II of the predicted EF-Tu$_{pl}$ protein, was used in an RNase protection assay to demonstrate the presence of *tufA* transcripts in total RNA extracted from erythrocytic parasites (Fig. 4).

Modelling of the three-dimensional structure of P.falciparum EF-Tu$_{pl}$.

Despite the highly divergent amino acid composition of Pf EF-Tu$_{pl}$, a computer model showed conservation of secondary structure motifs in all three domains of the hypothetical protein. The model is reliable, with good confidence in the overall folding and also in the detail of the secondary structure compared with *T.aquaticus*. Only minor differences were found in the length of some structural motifs: in domain I there are small length differences in 5 of the nine alpha helices and in 3 out of six β strands. The changes are more pronounced in domain II where the first two β-strands seem to be continuous in Pf, and an extra β-strand is formed by residues Gly245 - Leu249. In domain III, differences from *T. aquaticus* are again minor with a slightly different positioning of two β-strands.

The model for Pf EF-Tu$_{pl}$.GTP showed that the GTP-binding site is conserved as well as the whole lining towards the GTP-binding pocket. There is also conservation on the interface between the domains. These interfaces are exposed when EF-Tu. GTP converts to the effective EF-Tu.GDP form. In this form of the protein, conserved residues in the cleft between domains I and III correspond to the site

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which other studies have shown kirromycin binds.

5   The effects of three classes of compounds on intraerythrocytic parasites of
       P.falciparum in vitro, as well as on *P.chabaudi in vivo*, are considered below. In
       assessing the significance of these results it should be noted that in prokaryotes,
       kirromycin, whose binding site is at the interface of domains I and III of EF-Tu.GTP
       (Mesters *et al*. 1994), binds to the ternary complex of tRNA and EF-Tu.GTP
10   preventing the conformational change required for release from the ribosome upon
       GTP hydrolysis, whereas the drug has a different effect on eukaryotic cells. In the
       latter, at 100µM, it blocks RNA synthesis without affecting DNA or protein
       synthesis (Schmid *et al*. 1978).

15   **Kirromycin**: Kirromycin-resistant forms of bacterial EF-Tu are modified at one of
       seven amino acids along the opposing interfaces of domains I and III (Mesters et al
       1994 and Abdulkarim et al 1994) and Pf EF-Tu$_{pl}$ has a substitution at one of these
       sites (A375S-*E.coli* numbers) that could potentially confer resistance to kirromycin.
       To test this possibility, kirromycin (Mocimycin), its methylated derivative Aurodox
20   or its disaccharide derivative Efrotomycin were incubated with erythrocytic stages of
       P.falciparum grown in cultures over a 36 hr period. The incorporation of both ^{3}H-
       hypoxanthine and ^{14}C-isoleucine was inhibited in a dose-dependent fashion,
       maximum inhibition being achieved at 100µM kirromycin (Fig. 5). Similar levels of
       inhibition were obtained for all three compounds. In synchronized cultures,
25   inhibitory effects on ring stage parasites were observed as early as five hours after
       exposure to Aurodox and were maximal after 10 hrs exposure. Once maximal
       depression of incorporation had been reached at any particular dose of drug, residual
       incorporation continued at a uniform rate thereafter. Vital staining with rhodamine
       123, a fluorescent dye that concentrates within the mitochondrion (Divo *et al*. 1985)
30   confirmed the parasiticidal effect, loss of specific mt staining being evident within 2-
       3 hours (data not shown). Treatment of parasites with 1mM Aurodox for 1.5 cell

cycles, followed by removal of the antibiotic by washing and follow-up for 2 weeks *in vitro*, indicated the effect was parasite death rather than stasis. Blood cultures of *P.falciparum* were about 10 times more sensitive to the antibiotic than a gram-positive bacterium (*Corynebacterium spp*) used in parallel bioassays.

5

On the basis of these findings, preliminary studies were carried out on mice infected with *P.chabaudi*. In the first experiment, mice were infected and inoculated on the same day intraperitoneally with 0.1 ml of 100mM Aurodox, a dose calculated to mimic the maximal inhibitory effect observed *in vitro*. The Aurodox-treated animals

10   showed a lag in development of the infection compared with untreated controls indicating partial inactivation of the infectious inoculum (Fig. 6). In a single experiment. Mocimycin was found to be less effective *in vivo* than Aurodox.

Enacyloxin IIa: Enacyloxin IIa (ExIIa) is a linear antibiotic representing a new

15   family of polyenic antibiotics (Watanabe 1992) that bind to EF-Tu and block transfer to the nascent peptide chain of aminoacylated-tRNA bound at the A site (Cetin 1996). The profiles for inhibition of radiotracer incorporation in blood cultures of *P.falciparum* incubated with Ex IIa were similar to those with Mocimycin.

20   **GE2270:** This is a thiopeptide antibiotic in the same family as thiostrepton. It binds to a different site on Ef-Tu than kirromycin and locks the protein into a different conformation (Landini 1996). This antibiotic was more inhibitory in blood cultures than either kirromycin or thiostrepton (Fig. 5).

25   **Fusidic acid:** Fusidic acid, presently in clinical use as a narrow spectrum antibiotic, was assessed as a potential antimalarial by titration with *P.falciparum in vitro*, as described above. Maximum inhibition of radiotracer incorporation was achieved at a concentration of 200 µM (Fig. 5). Preliminary experiments with fusidic acid in mice infected with *P.chabaudi* found little effect on parasitaemias, even at toxic dose

30   levels of the drug.

Thiostrepton: Nucleotide (nt) sequences are available for the GTPase domain of the 28S rRNA specified by the nucleus (Rogers et al. 1996), as well as the 23S rRNAs specified by the mt and pl large subunit rRNA genes of the human malaria pathogen *Plasmodium falciparum* (Pf) (Feagin, 1992). These data indicate that the high affinity binding site for the thiazolyl peptide antibiotic thiostrepton, A_{1067} in *E.coli* (Thompson et al 1991, Ryan et al 1991 and Rosendahl et al 1994), is conserved in the GTPase domain encoded by the plastid DNA, but modified to a G in both nuclear and mitochondrial genomes (Fig. 7).

We have tested thiostrepton to ascertain whether it inhibits Pf and found reproducible inhibition of uptake of ^{3}H-hypoxanthine and ^{14}C-isoleucine in blood cultures (50% inhibition at 3-5μM thiostrepton). Onset of inhibition of protein synthesis by thiostrepton was more rapid (5 hrs) than by tetracycline (8 hrs). Specificity was demonstrated by the lack of effect of viomycin (data not shown), an unrelated antibiotic that also can inhibit translocation (Kutay et al 1990).

Having established thiostrepton's activity, we asked "does the antibiotic bind preferentially to the nuclear, mitochondrial or plastid forms of Pf 28/23S rRNA?". Evidence that the highest affinity interaction of thiostrepton is with 23S $rRNA_{pl}$ was obtained from an *in vitro* binding assay (Ryan et al 1991). Short transcripts of wild type (wt) RNA corresponding to the GTPase domain of Pf 23S $rRNA_{pl}$ (nts 987-1078) were transcribed *in vitro* from a PCR product that included a T7 promoter sequence in one of the primers. Mutated malarial rRNA sequences (*E.coli* numbers A1067U and A1067G) were obtained by PCR methodology and transcribed in the same way. Both wild type and modified transcript sequences were verified prior to thiostrepton binding assays. A positive control transcript was used based on the 23S rRNA sequence of *E.coli* with a mutation (U1061A) that increases stability and binding. Fig. 8A shows that the mutation Pf_{pl} (*E.coli* number A1067U) markedly reduced thiostrepton binding (~14% of wt). An intermediate level of binding (~35% of wt) was obtained with the mutation Pf_{pl} (*E.coli* number A1067G). Thiostrepton binding to a transcript corresponding to the GTPase domain (nt 1334-1427) of the

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cytosolic Pf 28S rRNA was ~10% of that for Pf 23S rRNA$_{pl}$. These data show that the nts crucial for thiostrepton binding to Pf 23S rRNA are as in *E.coli*, and that the plastid form has the highest binding affinity.

5   In the same way, we tested a transcript corresponding to the GTPase domain of the 23S rRNA$_{pl}$ of *Toxoplasma gondii* (Tg), a related apicomplexan that is an important opportunistic pathogen in patients with AIDS. In this case, the wild type sequence has a substitution at a different site (*E.coli* number A1077U) - see Fig. 7, that inhibits binding by thiostrepton in *E. coli* (Ryan et al 1991). This was found also to be the

10   case with a transcript derived from a PCR product covering the GTPase domain of Tg$_{pl}$ 23S rRNA (nt 926-1024) (Fig. 8B). Corrective mutation of the Tg$_{pl}$ transcript (*E. coli* number U1077A) conferred a significant increase (x5) in thiostrepton binding (Fig. 8B).

15   These thiostrepton binding studies constitute the first direct evidence that components of the malarial plastid organelle could be preferentially targeted by drugs. The results complement earlier studies (Pfefferkon *et al* 1994 and Beckers *et al* 1995) which inferred that toxoplasma's 23S rRNA$_{pl}$ might be the target of the macrolide antiobiotic, clindamycin, acting at a different effector site.

20

Drugs bind to heterologously expressed EF-Tu

The material *tufA* gene in pGEX was expressed as an insoluble fusion protein in *E.coli* JM 109. The protein was detected either with antibodies to the GST tag or

25   with antibodies to a specific peptide sequence in domain I (IQKNKDYELIKSN) not found on *E.coli* EF-Tu. Washed inclusion bodies were dissolved and refolded by dilution (Lin et al 1991). This yielded a small amount of refolded protein that migrated in native acrylamide gels as a spontaneously cleaved product and we used this to show that the expressed protein forms complexes with kirromycin and other

30   drugs that bind to different sites on EF-Tu. As shown in Fig. 13, the mobility (M$_r$) of the expressed malarial protein was advanced or retarded in these complexes in the

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same characteristic way described for *E.coli* EF-Tu (Cetin et al 1996): the M_r of the GDP form of the complex decreased with GE2270A, but increased with enacyloxin IIa or kirromycin. These results show that the heterologously expressed Pf EF-Tu$_{pl}$ can adopt a native conformation and bind the classical antibiotic inhibitors.

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